



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 12511

TO: Karen A Lacourriere

Location:

Art Unit: 1635

July 26, 2004

Case Serial Number: 09/301380

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes

18 Jul 2

Sheppard, Paula

From: Lacourciere, Karen
Sent: Wednesday, July 21, 2004 3:48 PM
To: Sheppard, Paula
Subject: RE: Sequence search

Hi Paula-
The numbers are
ABA70229
AAI50358
AAK44359
AAK18454
ABS44016
ABS18595
ABA71469
AAI51738
AAK45811

The serial number is 09/301,380 and the sequence these oligos bind to is SEQ ID NO:1
I can bring the original search down to you if it helps. Let me know what you need! Thanks so much, I really appreciate your help.
Karen

-----Original Message-----

From: Sheppard, Paula
Sent: Tuesday, July 20, 2004 5:28 PM
To: Lacourciere, Karen
Subject: RE: Sequence search

Yes. If you can provide the accession numbers of interest and the seq ID used to search it, then I can provide you with alignments and references.

Paula
(571) 272-2529

-----Original Message-----

From: Lacourciere, Karen
Sent: Tuesday, July 20, 2004 2:53 PM
To: Sheppard, Paula
Subject: Sequence search

Hi Paula-
You did a sequence search for me back in May on SN 301,380. Some of the hits which appear in the summary now appear to be potentially useful references, but they are too far down on the list and the detailed summaries were not provided. Is it possible to get more information on these sequences based on the accession numbers?
Thanks-
Karen

Karen A. Lacourciere Ph.D.
Remsen 2D15 GAU 1635
(571) 272-0759

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> O <
O | O IntelliGenetics
> O <
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FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file 1_x_listing_inv.res made by spaula on Mon 26 Jul 104 14:24:17-PDT.

```
Query sequence being compared:US-09-301-380-1' (1-4134)
8
Number of sequences searched: 8
Number of scores above cutoff: 8
```

Results of the initial comparison of US-09-301-380-1' (1-4134) with:

```
File : aa150358.seq
File : aa151738.seq
File : aak18454.seq
File : aak18459.seq
File : aak44359.seq
File : aak5811.seq
File : aba1469.seq
File : abs18595.seq
File : abs44016.seq
```

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The scores below are sorted by initial score.

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. aak18454	Human brain expressed single	230	230	0.57	0	-
2. aak14359	Human bone marrow expressed s	230	230	0.57	0	-
3. abs18595	Human Genome-derived single e	230	230	0.57	0	-
4. abs44016	Human liver single exon probe	230	230	0.57	0	-
5. aak15811	Human foetal liver single exon	224	224	0.49	0	-
6. aba1469	* *** 1 standard deviation below mean	224	224	0.49	0	-
7. aai150358	TOIG of: aai150358 check: 446	611	55	289	-1.50	0
8. aa151738	TOIG of: aa151738 check: 878	697	35	287	-1.73	0

1. US-09-301-380-1' (1-4134)
aa18454 Human brain expressed single exon probe SEQ ID NO:

TOIG of:	aa18454	check:	7397	from:	1	to:	230
ID	AAK18454	standard; DNA; 230 BP.					
XX							
AC	AAK18454;						
XX							
DT	05-NOV-2001	(first entry)					
XX							
DB	Human brain expressed single exon probe SEQ ID NO: 18445.						
XX							
KW	Human; brain expressed exon; gene expression analysis; probe: microarray;						
KW	Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;						
ss.							
XX							
OS	Homo sapiens.						
XX							
PN	WO200157275-A2.						
XX							
PD	09-AUG-2001.						
XX							
PR	30-JAN-2001; 2001WO-US000667.						
XX							
PR	04-FEB-2000; 2000US-0180312P.						
PR	26-MAY-2000; 2000US-0207456P.						
PR	30-JUN-2000; 2000US-0060840B.						
PR	03-AUG-2000; 2000US-00632366.						
PR	21-SEP-2000; 2000US-023487P.						
PR	27-SEP-2000; 2000US-0236359P.						
PR	04-OCT-2000; 2000GB-00024263.						
PA	(MOLE-) MOLECULAR DYNAMICS INC.						
XX							
PI	Penn SG, Hanzel DK, Chen W, Rank DR;						
XX							
DR	WPI; 2001-483446/52.						

PARAMETERS

Similarity matrix	Unitary	K-tuple	
Mismatch penalty	1	Joining penalty	4
Gap penalty	1.00	Window size	30
Gap size penalty	0.33		500
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	182	225	84.92

PT

Total Elapsed
00:00:00.00

PS

Example 4; SEQ ID NO 1B445; 650pp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention

XX

XX (MOLE-) MOLECULAR DYNAMICS INC.
 XX PA
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX PI
 XX DR WPI; 2001-488898/53.
 XX Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human adult liver.
 XX PT
 XX PS Claim 4; SEQ ID NO 19006; 658pp; English.
 XX CG
 XX CG
 CC present sequence is a single exon probe open reading frame of the
 CC invention. Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp://wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
 ABS18595 Length: 230 July 26, 2004 14:11 Type: N Check: 7397 ..

Initial Score = 230	Optimized Score = 230	Significance = 0.57
Residue Identity = 100%	Matches = 230	Mismatches = 0
Gaps = 0	Conservative Substitutions = 0	

XX DE Human foetal liver single exon nucleic acid probe #19774.
 XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX OS Homo sapiens.
 XX PN WO20015777-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JAN-2001; 2001WO-US000669.
 XX PR 04-FEB-2000; 2000US-0180312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX PR 30-JUN-2000; 2000US-00632368.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0236559P.
 XX PR 27-SEP-2000; 2000US-0236559P.
 XX PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLB-) MOLECULAR DYNAMICS INC.
 XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2001-483447/52.
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX PS Claim 4; SEQ ID NO 19774; 639bp + Sequence Listing; English.
 XX XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 224 BP; 58 A; 59 C; 49 G; 58 T; 0 U; 0 Other;
 XX AB71469 Length: 224 July 26, 2004 14:11 Type: N Check: 7602 ..
 XX Initial Score = 224 Optimized Score = 224 Significance = 0.49
 Residue Identity = 100% Matches = 224 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0
 XX 1450 1460 1470 1480 1490 X 1500 1510
 TACTGTCACACATTACACCGCACGTTCCAGGAGCCACATTGGGAGGTCTCAGAATGTCATGA
 X 10 20
 XX 1590 1600 1610 1620 1630 1640 1650
 GCCTGCCCTGAGAAATAATTGGATCATTTGCACACAGATGTCATCATCACCATCTTCT
 CTACAGCTGGCTGAGAAATAATTGGATCATTTGCACACAGATGTCATCATCACCATCTTCT
 X 30 40 50 60 70 80 90
 XX 1660 1670 1680 1690 1700 1710 1720 1730
 GGCGCCCACTTAACATTGTAAGGGCTTGCCCCATTAGATTCAGAACCATGAAAGGGCTTCAGGTAACT
 GCCTGCCCTGAGAAATAATTGGATCATTTGCACACAGATGTCATCATCACCATCTTCT
 CTACAGCTGGCTGAGAAACAACCCAACTGTCATTCAAGGTGATAGGTGAAACAGGTG
 X 100 110 120 130 140 150 160
 XX 1740 1750 1760 1770 1780 1790 1800 1810
 CCAAATPATCAGGCTCTGATCCAGTCAGTCATCATCACCATCTTCT
 AA150358 7. US-09-301-380-1' (1-4134) TOIG of: aa150358 check: 4462 from: 1 to: 611
 LOCUS AA150358 611 bp mRNA linear EST 14-MAY-1997
 DEFINITION 2107a03 r1 Soares_pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:41596 5', mRNA sequence.
 ACCESSION AA150358
 VERSION AA150358.1 GI:1721870
 KEYWORDS EST, Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 611)
 AUTHORS Hillier L., Lennon G., Becker M., Bonaldo M.F., Chiappelli B., Chissoe S., Dietrich N., Dubroque T., Favello A., Gish, W., Hawkins M., Holtzman M., Kucaba T., Lacy M., Le N., Mardis E., Moore B., Morris M., Parsons J., Prague C., Riekin, L., Rohlfing T., Scheibenbogen K., Soares M.B., Tan P., Thierry-Mieg J., Travaskis E., Underwood K., Wohldmann P., Waterston R., Wilson R., and Marra M.
 TITLE Generation and analysis of 280,000 human expressed sequence tags
 JOURNAL Genome Res. 6 (9), 807-828 (1996)
 MEDLINE 97044478
 PUBMED 8883549
 COMMENT Contact: Wilson RK Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LinkL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.
 Insert Length: 1102 Std Error: 0.00
 Seq Primer: -28M13 rev3 from Amersham
 High Quality sequence stop: 328.
 FEATURES Location.Qualifiers
 source 1..611
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:3806183"
 /db_xref="taxon:9616"
 /clone="IMAGE:41596"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_idb="Soares_pregnant_uterus_NbHPU"
 /note="Organ: uterus; Vector: PT73-Pac; Site 1: Not I - Oligo(dT) primer [5', AACCGAAACATTGCGGCCCTTTTTTTTTTTTT 3', 1, double-stranded DNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified PT73 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
 AA150358 Length: 611 July 26, 2004 14:10 Type: N Check: 4462 ..
 Initial Score = 55 Optimized Score = 289 Significance = -1.50
 Residue Identity = 50% Matches = 391 Mismatches = 210
 Gaps = 175 Conservative Substitutions = 0
 XX 2860 2870 2880 2890 2900 X 2910 2920
 TTGGGGTTGCCATTAGCTCTGGGACAGCACAAAGATTGAGGGC
 170 180 190 200 210 220 X ||| ||| ||| |||

1540 1550 1560 1570 1580 1590 1600
 AACCCCATGTCATCAGGGCTGAACTTGTGATGGTAT-GAACAAAGTTGGTGCAGACATA
 ATTCAAAATTGTTCCAAAGGNN
 20 30 40 50 60 70 80
 1610 1620 1630 1640 1650 1660 1670
 TTGGATAACATTTGCCAACACCACAGATGTTCCATTCACTACCATCCTTGCGCOAGCTAACATTGTA
 NNNG-NNNAT--CC----CNGAANTAGATTCTGATGTT-----CTGTGT-----CTAAGATTCTA
 90 100 110 120 130
 1680 1690 1700 1710 1720 1730 1740
 CGAAAGGCCATTAGATTCGAAACATCAAGGCTTCCAGTAATTCCTAAATTATAAGGCTCTGA
 -GATCAGATGTCCTAGATGTTAA-----TA-----AGATTAACTGGCTGT
 140 150 160 170 180
 1750 1760 1770 1780 1790 1800 1820
 TCCAGTCCTCCACAGTGTGGGTTTATCTGGTTCTGGCTTCTGGCTCAAATACCTGCTCAGACGGCTC
 T---CTGT-TT-GAGGACTCTAGATTCTAT-TGGTCC-AAGATTCTGG-----GATCCT-----AAGNATC
 190 200 210 220 230
 1830 1840 1850 1860 1870 1880 1890
 GCTGGG-GAAGCTC---TTCCCAATGCGTCACTGCCATCACGGAGAGGAGTACTCACTGAA
 NAGGGANAGAGNCACNCAACNAGNNAGGNNAGAGANCAAAAGGAAAATA-ANGTCAANGNTGGACACC
 240 250 260 270 280 290 300
 1890 1900 1910 1920 1930 1940 1950
 TGATCTCATA-TTCGATG---ATGAATTGTAATGGCTATGTTGCACTGCTGGCTGCA
 NNAGGGCTTGTGCAATTCTGCTAGACCAT-GTTAA-GCTAAATGTTCTAAAGATTCTAA-
 310 320 330 340 350 360 370
 1960 1970 1980 1990 2000 2010 2020
 TGATCTCATA-TTCGATG---ATGAATTGTAATGGCTATGTTGCACTGCTGGCTGCA
 --ATCTT-ATAGTCTAGGACTGTA-GTCTAA-GACTAAATGTTCTAAAGATTCTAA-
 380 390 400 410 420 430 440
 2030 2040 2050 2060 2070 2080 2090 2100
 CTGAAACACTTGTCAACTTGATCTGTCAGTTCTAACTGCAAGGGAGGATTTGGCATCGTAAACGGAGC
 GTCACA---GTTCTAG---ACTATTAGTGCATTCAAGG-----TTCTAAC--CTTAACTGTGAT
 450 460 470 480 490
 2110 2120 2130 2140 2150 2160 2170
 TGAGGTGAGTAGGCAACACGCTGAACTGTCAGTCAGCTGCTGGAGAGCTGCTGTCAGTCA
 ATTCCTGGGT-GCCCTCTCTCTAG-TATC-ATTCGTCCT-CCTCCCA-ATCTG---TGG---
 500 510 520 530 540 550
 2180 2190 2200 2210 2220 2230 2240
 ACAGTGTAGGCTCCGCTGTCATGTCAGCATCCTACACTAGATG-ATCCCTGTCACAG-TGAA
 ---GGGT---GTCCTCTCTAG-TGGCTGCAAT-GC-ATTA-GGGATGCTCCCTTCGGAGATGGA
 560 570 580 590 600 610
 2250 2260 2270 2280 2290 2300 2310
 CCTTTTCATCCTGGCACTTCTGTCAGCTGTCAGCTGAGGAGATAGGTGTGATCATGTT
 CGATTCTACCTTTC-EGGCTATG-TGCTCGAGGCATCCCACCTCTGAGA-NAGATGATC-TGGC
 620 630 640 650 660 670 680
 2320 2330 2340 2350 2360 2370
 TCACCTTCATCCTGGCACTTCTGTCAGCTGTCAGCTGAGGAGATAGGTGTGATCATGTT
 TCAAGGGGNAGTCAX
 690 X

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O|O IntelliGenetics
> O <
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 1_x_listing.res made by spaula on Mon 26 Jul 104 14:22:49-PDT.

		PARAMETERS		SEARCH STATISTICS		FEATURES	
		Score:	Mean	Median	Standard Deviation	Source	Location/Qualifiers
Similarity matrix	Unitary	K-tuple	4			1. .611 /organism="Homo sapiens" /mol_type="mRNA"	
Mismatch penalty	1	Joining Penalty	30			/db_xref="GDB:13806183"	
Gap penalty	1.00	Window size	500			/db_xref="ITAXON:9606"	
Gap size penalty	0.33					/clone="IMAGE:491596"	
Cutoff score	0					/sex="female"	
Randomization group	0					/dev_stage="adult"	
STDEV	-2					/lab_host="DHIOB"	
						/clone_id="Soares_Pregnant_uterus_NbHPG"	
						/note="Organ: uterus; Vector: pRT73-Paci Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5,"	
Number of residues:							
Number of sequences searched:							
Number of scores above cutoff:							
Number of scores above cutoff:	57	Mean	57	72	20.44	Total Elapsed	8
Times:		CPU	00:00:00.00		00:00:00.00		
Number of residues:						2676	
Number of sequences searched:						8	
Number of scores above cutoff:							
The scores below are sorted by initial score.							

Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init.	Opt.	Sig.	Frame
1. aa150358	TOIG of: aa150358 check: 446 Human brain expressed single	611	77	280	0.98	0	
2. aak18454	Human bone marrow expressed s	230	71	111	0.68	0	
3. aak4359	Human genome-derived single e	230	71	111	0.68	0	
4. abs18595	Human liver single exon probe	230	71	111	0.68	0	
5. abs44016	Human bone marrow expressed s	224	38	107	0.93	0	
6. aak45811	Human foetal liver single exo	224	38	107	0.93	0	
7. aba71469	***** 1 standard deviation below mean	224	38	107	0.93	0	
8. aa151738	TOIG of: aa151738 check: 878 697	25	294	-1.57	0		
1. US-09-301-380-1 (1-4134)							
aa150358	TOIG of: aa150358 check: 4462 from: 1 to: 611						
TOIG of: aa150358 check: 4462 from: 1 to: 611							
LOCUS AA150358	611 bp mRNA linear EST 14-MAY-1997						
DEFINITION z107403.r1 Soares_Pregnant_uterus_NbHPU Homo sapiens cDNA clone IMAGE:491596 5' mRNA sequence.							
ACCESSION AA150358							
VERSION AA150358.1	EST						
KEYWORDS SOURCE Homo sapiens (human)							
ORGANISM Homo sapiens							
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.							
REFERENCE 1 (bases 1 to 611)							
AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubroca,T., Favrello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Riffkin,J., Schellenberg,K., Tan,F., Thierry-Mieg,J., Trevisakis,E., Underwood,R., Wohldmann,P., Waterston,R., Wilson,R., and Marra,M.							
TITLE Generation and analysis of 280,000 human expressed sequence tags							
JOURNAL Genome Res.	6 (9), 807-828 (1996)						
MEDLINE 97044478							
PUBMED 8889549							
COMMENT Contact: Wilson RK							
Washington University School of Medicine							
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108							
Tel: 314 286 1800							
Fax: 314 286 1810							
Email: est@watson.wustl.edu							
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.							
Insert length: 1102	Seq primer: -28M13 rev2 from Amersham	3rd Error: 0.00					
High quality sequence stop: 328.							
FEATURES Location/Qualifiers							
1. .611							
/organism="Homo sapiens"							
/mol_type="mRNA"							
/db_xref="GDB:13806183"							
/clone_id="Soares_Pregnant_uterus_NbHPG"							
/note="Organ: uterus; Vector: pRT73-Paci Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5,"							

AACTGGAGAATTCGCGCCCTTTTTTTTTT 3',
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pRIT3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."

ORIGIN

AAT50358 Length: 611 July 26, 2004 14:10 Type: N Check: 4462 ..

Initial Score = 797	Optimized Score = 280	Significance = 0.98	
Residue Identity = 130	Matches = 363	Mismatches = 0	
Gaps = 20	Conservative Substitutions = 237		

700 710 720 730 740 750 760
AGAGTTCTCAAGGGACCTTGATGGGACTTATTTCATGCCTCCAGAGGACACCCTGAT
X AAGAAC-CAGGGCTTAG--AT
X 10

770 780 790 800 810 820 830
ATCTGTATGCTAGATTAATCATCTAACCATACAGCAGAGCAACCTATTCTCTGGAAGGTGATTCA
TCTTTAG-TACA-TTGTGTT---GATGTTCCACAGAAC-ACT-T-----AAG-TGTATACT
20 30 40 50 60 70

840 850 860 870 880 890 900
GTCGATGATGATGATGACACTATAGCTGTAAT-TTG-AGTGACACTGAGTTTATGGCTAAATCAGTA
GTTG-TG---TAATGTCCTCTGAAAGG -AACCTGTCTAAACCTGGTT-TGCTGTTTGGAGTT
80 90 100 110 120 130

910 920 930 940 950 960 970
GAGAGGOCACCAATTTAACTCCAGAAGCA-ATGCAAGTAACAGAGGAATTAGCGGAATATGTC
TCATA---CCTRAAAATCATTTT-----GGTATATCCTGATAATCTCTA-TAA-TACTA-GAATTGT
140 150 160 170 180 190

980 990 1000 1010 1020 1030 1040
CTTCACTGGAGTGCATGAGAGGACTGCCAACCAAATTATTACTGGCAAAGGAGATGGCTA
CT-GCA---AAATATAGT-AAGAGAATG--GAGCTTAAT-----AGCT-GATTCCT-
200 210 220 230

1050 1060 1070 1080 1090 1100 1110
CCCCAAAACAGGACAGTTATAAAGACTTTGAGAAACCTGGAGATCATGTTCAAGGCAGACTCT
CCCA-ATTTA-TCTG-TTAT---GTTTGTACTA--TT-CACAT-TTATGCTTT---TC-TACGAT
240 250 260 270 280 290

1120 1130 1140 1150 1160 1170 1180
GGAAATTAACCAATGTA-TAGCAAAAATGATTAGGACCATCACCATACTTGTAGAGTTAACGC
AAAATGTTGATTTGATGCCA-GTA-TAGGAACCTCAATC-TTGTGTTTGTGCTTAAAGA
300 310 320 330 340 350

1200 1210 1220 1230 1240 1250 1260
GGCTCCATACTGGATCACGGCCCTCAAATCTGGTGTG-CTGCCCCAGAGGATGGACCTTGATC-TGC
AGGTTCAGT-TGTT-GATTAAAGTTC--TCCPA-AATTAGAATGCCAATCTATGTAATAACCTAG-GCAT
360 370 380 390 400 410 420

1270 1280 1290 1300 1310 1320
AGAGCT---ATGGCAACCCAAACCGAAATTAGCTGGTAAACAATGGATCCAAATGAAATGCCC
CAAGCTGAAATTAAAGTTC--TCCPA-AATTAGAATGCCAATCTATGTAATAACCTAG-GCAT
430 440 450 460 470 480 490

1330 1340 1350 1360 1370 1380 1390
GATGCAACCCAAACCGAAATTAGCTGGTAAACAATGGATCCAAATGAAATGCCC
GA-GTCCCTAG-GGAGAGTAAATGCA-NTGGTAAAGTGC--TTTTAGTA-AAGGTGTCNGTA
500 510 520 530 540 550

1410 1420 1430 1440 1450 1460 1470
TATCAGTGAATGCTCTPATGATGATATTGATATTACTGGCA-AACGCAATTGAAATGCTGCTAGC
TGTC-CTGATTTGACATAAGGATA-GACCTGGCAGGAGAA--ATAAGTAAAG
560 570 580 590 600 610

1480 1490 1500
CACCAAGATCCCTCACACTGCAAACACTCTAACAG
XX DT 05-NOV-2001 (first entry)
Human brain expressed single exon probe SEQ ID NO: 18445.
aaK18454

ID AAK18454 standard; DNA; 230 BP.
XX AC AAK18454;
XX XX

700 730 740 750 760
TOIG of: aak18454 check: 7397 from: 1 to: 230

XX OS Homo sapiens.
XX PN WO200157275-A2.
XX PR 04-OCT-2000; 20000US-0207156P.
PR 26-MAY-2000; 20000US-0180312P.
PR 04-FEB-2000; 20000US-0180312P.
PR 30-JUN-2001; 20001WC-US000667.
PR 03-AUG-2000; 20000US-0063308.
PR 21-SEP-2000; 20000US-00633366.
PR 27-SEP-2000; 20000US-0236339P.
PR 04-OCT-2000; 20000GB-00024263.
XX PA (MOLE-) MOLECULAR DYNAMICS INC.
XX PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX DR WPI; 2001-483446/52.

XX PT Single exon nucleic acid probes for analyzing gene expression in human
PT brains.
XX PS Example 4; SEQ ID NO 18445; 650pp + Sequence Listing; English.
XX CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is one of the probes of the
CC invention.
XX SQ Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;
XX PS Initial Score = 71 Optimized Score = 111 Significance = 0.68
Gaps Residue Identity = 52% Matches = 139 Mismatches = 0
PS AAK18454 Length: 230 July 26, 2004 14:10 Type: N Check: 7397
420 430 440 450 460 470 480
GAAACGGTCATTTAAACATCATGAGGAAGGGTACCTATGAGGACTT-CAGTGACAGC

		Gaps	=	4.2 Conservative Substitutions	=	0
XX	Homo sapiens.					
OS						
XX	WO200186003-A2.					
PN						
XX	15-NOV-2001.					
XX	30-JAN-2001; 2001WO-US000665.					
PF						
XX	04-FEB-2000; 2000US-0180312P.					
PR	26-MAY-2000; 2000US-0207458P.					
PR	30-JUN-2000; 2000US-00608408.					
PR	03-AUG-2000; 2000US-00632366.					
PR	21-SEP-2000; 2000US-0234687P.					
PR	27-SEP-2000; 2000US-02363595.					
PR	04-OCT-2000; 2000GB-00024263.					
XX	(MOLE-) MOLECULAR DYNAMICS INC.					
PA						
XX	Penn SG, Hanzel DK, Chen W, Rank DR;					
XX	WPI; 2002-114183/15.					
XX	Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.					
PT						
PT						
XX						
PS	Claim 4; SEQ ID NO 18586; 634pp; English.					
XX	The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes ; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarray having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangiomyomatosis, pulmonary alveolar proteinosis, Karagene syndrome, fibrocytic pulmonary dysplasia, primary ciliary dyskinesia, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe open reading frame of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences					
XX	Sequence 230 BP; 45 A; 61 C; 44 G; 80 T; 0 U; 0 Other;					
XX	Initial Score = 71 Residue Identity = 52% Optimized Score = 111 Matches = 139 Significance = 0.68 Mismatches = 84					
XX	(MOLIE-) MOLECULAR DYNAMICS INC.					
XX	XX PI Penn SG, Hanzel DK, Chen W, Rank DR;					
XX	XX PR 04-FEB-2000; 2000US-0180312P.					
XX	PR 26-MAY-2000; 2000US-0207458P.					
XX	PR 30-JUN-2000; 2000US-00608408.					
XX	PR 03-AUG-2000; 2000US-00632366.					
XX	PR 21-SEP-2000; 2000US-0234687P.					
XX	PR 27-SEP-2000; 2000GB-00024263.					
XX	PR 04-OCT-2000; 2000GB-00024263.					

2740 X 2750 2760 2770 2780 2790
 CATTCAAGGG
 CATTCAAGCTAACGGTATCGGATTACTATTGGAGAACCCAGAGTCATAA
 220 X

7. US-09-301-380-1 (1-4134)
 ab71469 Human foetal liver single exon nucleic acid probe
 TOIG of: ab71469 check: 7602 from: 1 to: 224
 ID ABA71469 standard; DNA; 224 BP.
 XX
 AC ABA71469;
 XX DT 01-FEB-2002 (first entry)
 XX DE Human foetal liver single exon nucleic acid probe #19774.
 XX KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX OS Homo sapiens.
 XX PN WO20015277-A2.
 XX PD 09-AUG-2001.
 XX
 30-JAN-2001; 2001WO-US000669.
 XX PF 04-FEB-2000; 2000US-0160312P.
 XX PR 26-MAY-2000; 2000US-0207456P.
 XX DR 30-JUN-2000; 2000US-00608408.
 XX PR 03-AUG-2000; 2000US-00632366.
 XX PR 21-SEP-2000; 2000US-0234687P.
 XX PR 27-SEP-2000; 2000US-02326359P.
 XX PR 04-OCT-2000; 2000US-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 XX DR
 XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
 CC human gene expression in a sample derived from human foetal liver.
 XX
 XX Claim 4; SEQ ID NO 19774; 63pp + Sequence Listing; English.
 CC The invention relates to a single exon nucleic acid probe for measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp://ftpi.wipo.int/pub/published_pct_sequences](http://ftpi.wipo.int/pub/published_pct_sequences)
 XX SQ Sequence 224 BP; 58 A; 59 C; 49 G; 58 T; 0 U; 0 Other;
 ABA71469 Length: 224 July 26, 2004 14:11 Type: N Check: 7602 ..
 Initial Score = 38 Optimized Score = 107 Significance = -0.93
 Residue Identity = 54% Matches = 134 Mismatches = 77
 Gaps = 37 Conservative Substitutions = 0

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 TACAAAGTTAGCTGGCAGAAGATGGATGATGAATGGACATCTGTGCTGGCAATGTCCA--
 X TCTCTCAGARTGT-CCGARG X 10 20
 2530 2540 2550 2560 2570 2580 2590 2590

AATATA-TTGTCCTAGGCCACGCCAA-CCTTTGT-TTCCA-TACCTGATCAAAGTCAAGGCCTGAAATGACAT
 ACTACAGCTGACTCGGG--GCCAACCCATGTCATTCAGGCCCTGAACTTGTATAAGTTGGAA--ACA-
 30 40 50 60 70 80
 2600 2610 2620 2630 2640 2650 2660
 GGTTGTC--CCCGAGGCCAGCTGAGCTCATGG-GACATCTGAAAGAACCTCCAAATGGTGCCTCCMCG
 90 100 110 120 130 140
 AGGTGGCTGGCTAGACA-ATATT--TGGATACATTGCCACAA----CCACAGATG-TCCATT
 150 160 170 180 190 200 210
 GAACGGCGGTGAACTGGTGGAAAGG-TACCTTAG-CCGAGGTCACCTGGACCAGAACCTCTGAAAG
 CATCATACCATCTTCTGGG-CGAGTACTTGTAGAG-GC-CRGG--CCATAGAT-TCGAAC
 2740 X 2750 2760 2770 2780 2790
 CATCCAGGACACCPACAAAGGCTATGGATTACTATGGAAAGCCAGAGTTCACTAA
 CATTCAGGG
 220 X

8. US-09-301-380-1 (1-4134)
 aa151738 TOIG of: aa151738 check: 8787 from: 1 to: 697
 TOIG of: aa151738 check: 8787 from: 1 to: 697
 LOCUS AA151738 697 bp mRNA linear EST 14-MAY-1997
 DEFINITION Z128n03.r1 Soares_pregnant_uterus_nbhp Homo sapiens cDNA clone
 IMAGE:5.03255' similar to contains element MER22 repetitive
 element ; mRNA sequence.
 ACCESSION AA151738
 VERSION AA151738.1 GI:1720293
 KEYWORDS EST
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 697)
 AUTHORS Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
 Chissoe,S., Dietrich,N., DubBugre,T., Favello,A., Gish,W.,
 Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
 Mardis,E., Morris,B., Morris,M., Parsons,J., Prange,C., Rieffin,L.,
 Rohling,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
 Trevaskis,B., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
 and Marra,M.
 TITLE JOURNAL
 MEDLINE Generation and analysis of 280,000 human expressed sequence tags
 9704478
 PUBMED 8889549
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LINL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
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 Seq Primer: -28M13 rev2 from Amersham
 High quality sequence stop: 513.
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 /db_xref="Taxon:9666"
 /clone="IMAGE_503265"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"

/clone lib="Soares pregnant uterus NBPHU"
 /note="Organ: uterus; Vector: pT7-*p*; Site 1: Not I;
 Site 2: Eco RI; 1st strand cDNA was primed with Not I -
 oligo(dT) primer [5'
 PAACTGGAGAATTCGGCCGCCTTTTTTTTTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT7 vector. Library
 went through one round of normalization. Library
 reconstructed by M. Batista-Bonaldo."